

10 30 50
-88 GTTGTCTGGGCAGCCAAGTTGGCATAATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29

70 90 110
-28 CCCTGCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGTCGCTCCACGTCT 31
-8 M A W L G A S L H V W 11

130 150 170
32 GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA 91
12 G W L M L G S C L L A R A Q L D S D G T 31

190 210 230
92 CCATCACTATAGAGGAGCAGATTGTCTTGTGTGTAAGCGAAAGTACAATGTGAACITCA 151
32 I T I E E Q I V L V L K A K V Q C E L N 51

250 270 290
152 ACATCACAGCTCAACTCCAGGAGGAGAGTAATTGTTCCCTGAATGGGATGGACTCA 211
52 I T A Q L Q E G E G N C F P E W D G L I 71

310 330 350
212 TTTGTTGGCCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATT 271
72 C W P R G T V G K I S A V P C P Y I Y 91

370 390 410
272 ATGACTTCAACCATAAAGGAGTTGCTTCCGACACGTGAACCCCAATGGAACAATGGGATT 331
92 D F N H K G V A F R H C N P N G T W D F 111

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

332	TTATGCACAGCTTAAATAAAACATGGGCCAATTATTACAGACTGCCCTTCGCTTCTGCAGC	430	450	470	391
112	M H S L N K T W A N Y S D C L R F L Q P				131
392	CAGATATCAGCATAGGAAAGCAAGAAATCTGTGAACGCCTCTATGTAATGTATACCGTTG	490	510	530	451
132	D I S I G K Q E F C E R L Y V M Y T V G				151
452	GCTACTCCATCTCTTTTGGTTCCCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGAC	550	570	590	511
152	Y S I S F G S L A V A I L I I G Y F R R				171
512	GATTGCATTGCAC TAGGA ACTATATCCACATGCAC TTA TTTG TGTCTTTTCATGCTGAGAG	610	630	650	571
172	L H C T R N Y I H M H L F V S F M L R A				191
572	CTACAAGCATCTTTGTCAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG	670	690	710	631
192	T S I F V K D R V V H A H I G V K E L E				211
632	AGTCCCTAATAATGCAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGACAAAT	730	750	770	691
212	S L I M Q D D P Q N S I E A T S V D K S				231
790		810	830		

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

692	CACAATATATCGGGTGAAGATTGCTGTTGTGATGTTTATTACTTCCTGGCTACAAATT	751
232	Q Y I G C K I A V V M F I Y F L A T N Y	251
752	ATTATTGGATCCTGTGGGAGGTCTCTACCTGCATAATCTCATCTTTTGCGCTTCTTTT	811
252	Y W I L V E G L Y L H N L I F V A F F S	271
812	CGGACACCAATAACCTGTGGGGCTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTTG	871
272	D T K Y L W G F I L I G W G F P A A F V	291
872	TTGCAGCATGGGCTGTGGCAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG	931
292	A A W A V A R A T L A D A R C W E L S A	311
932	CTGGAGACATCAAGTGGATTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA	991
312	G D I K W I Y Q A P I L A A I G L N F I	331
992	TTCGTCTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG	1051
332	L F L N T V R V L A T K I W E T N A V G	351
1052	GGCATGACACAAGGAAGCAATACAGGAACTGGCCAAATCGACACTGGTCTGTGCTCTAG	1111
352	H D T R K Q Y R K L A K S T L V L V L V	371

MATCH WITH FIG. 1D

FIG. 1C

1112	TCITTTGGAGTGCATTACATCGTGTTCGTGCTGCCTCACTCCTTCACTGGGCTCGGGT	1210	1230	1250	1171
372	F G V H Y I V F V C L P H S F T G L G W				391
1172	GGGAGATCCGCATGCACCTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTCTTTGTGICTA	1270	1290	1310	1231
392	E I R M H C E L F F N S F Q G F F V S I				411
1232	TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT	1330	1350	1370	1291
412	I Y C Y C N G E V Q A E V K K M W S R W				431
1292	GGAATCTCTCCGTGGACTGGAAAGGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAG	1390	1410	1430	1351
432	N L S V D W K R T P P C G S R R C G S V				451
1352	TGCTCACCACCGTGACGCACAGCACCGAGCCAGTCACAGGTGGCGGCAGCACACGCAT	1450	1470	1490	1411
452	L T T V T H S T S S Q S Q V A A A H A W				471
1412	GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC	1510	1530	1550	1471
472	C L S L A K L P R S P A D S L T A T S L				491

FIG. 1D

MATCH WITH FIG. 1D

1472	TTTACCTGGCTATGCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA	1570	1590	1610	1531
492	Y L A M S G V T Q S R T A S H T L S T R				511
1532	GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAGCCTTCCA	1630	1650	1670	1591
512	S N K E D S G R Q R D D I L M E K P S R				531
1592	GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT	1690	1710	1730	1651
532	P M E S N P D T E G				541
1652	GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAATGGCTGTTGTGTGAGAGGGC	1750	1770	1790	1711
1712	TTGGCTGATACCTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA	1810	1830	1850	1771
1772	TAATAGTTTTTAGGCTCCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG	1870	1890	1910	1831
1832	TGTC AATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT	1930	1950	1970	1891
1892	GGTATTGCTCTGTGATTGTTCA	1990			1914

FIG.1E

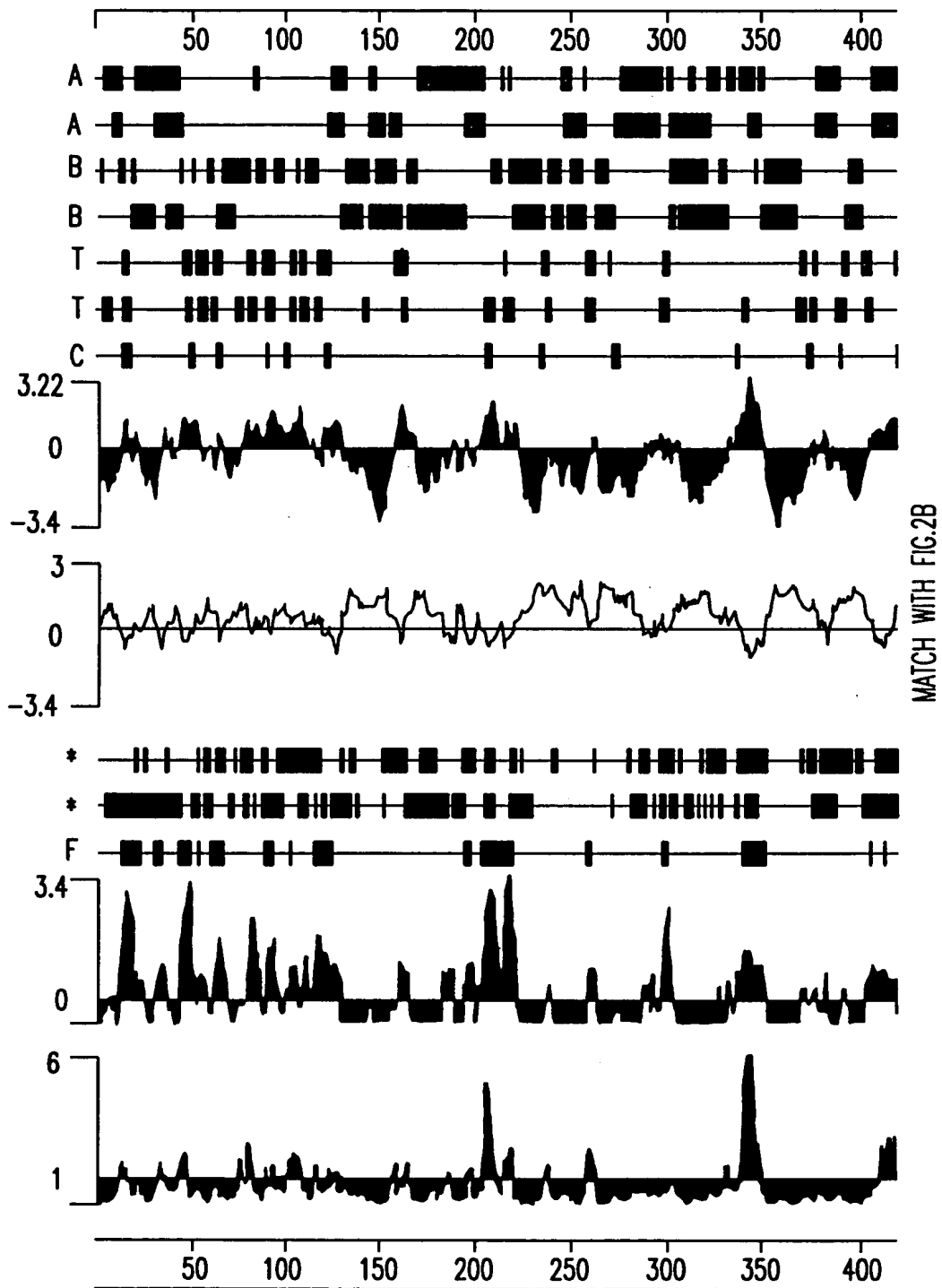


FIG. 2A

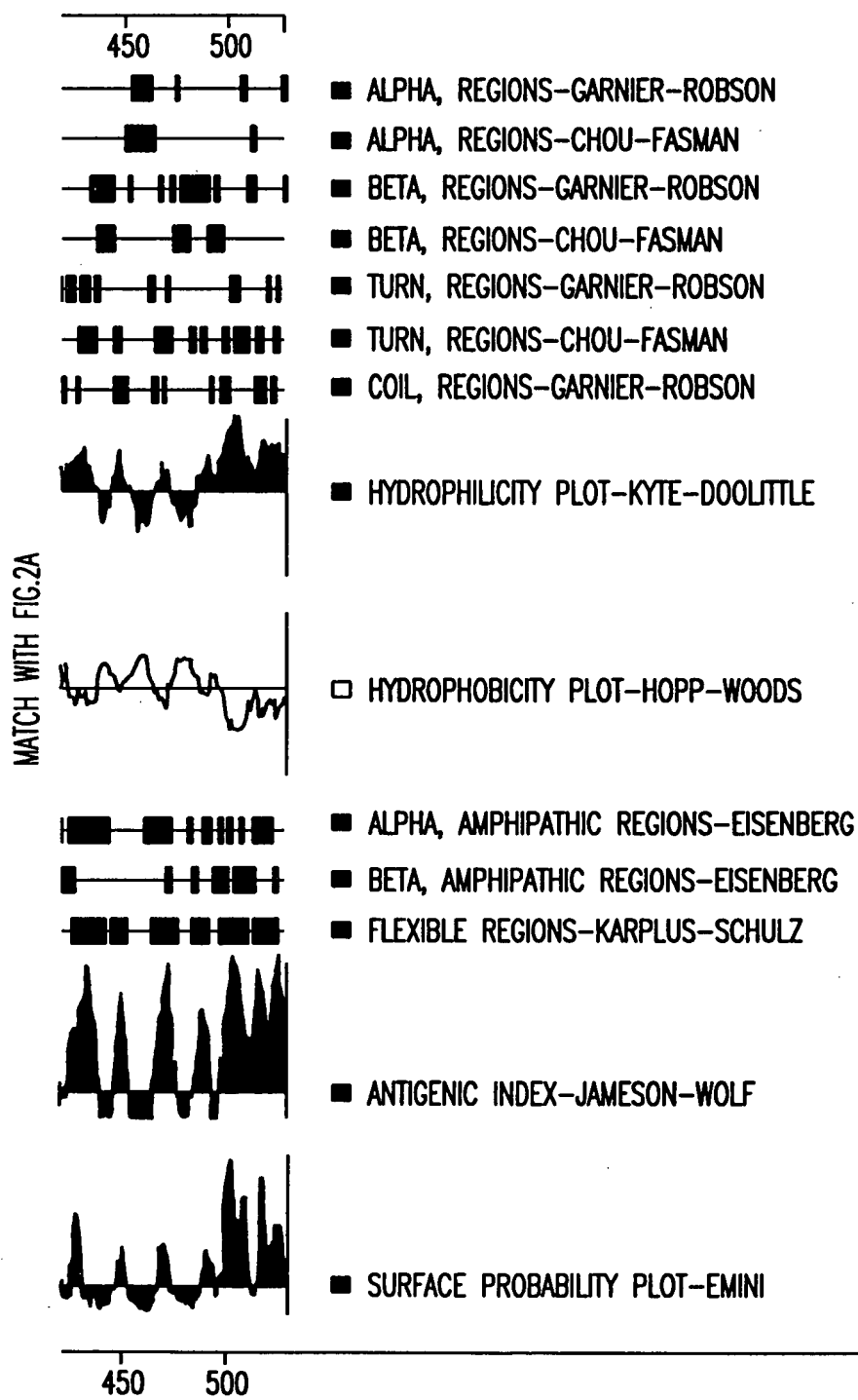


FIG. 2B

Sequences producing High-scoring Segment Pairs:			Reading High Probability	
			Frame Score	P(N)
gp M74445 OPOPTH1	parathyroid hormone receptor [Di...	+3	597	8.2e-204
pir S A39286	parathyroid hormone / parathyroid...	+3	597	2.9e-203
gp L04308 HUMPTH1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189
gp M77184 RATPATHYR1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188
gp X78936 MMPHRPR1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188
gp L34611 MUSPTH061	parathyroid hormone/parathyroid ...	+3	576	4.1e-174
gp U11087 HSV1RG91	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98
gp M86835 RATVASREC1	vasoactive intestinal polypeptid...	+3	254	3.1e-91

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG. 3A

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSDVKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLNLIFFAFFSDT 908
I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLNLIFFAFFS+
Sbjct: 253 ITEELRAFTPEPPADKAGFVGCRAVTVFLYFLTNNYYWILVEGLYLNLIFFAFFSEK 312

Query: 909 KYLWGFILIGWFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFIIF 1088
KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFIIF
Sbjct: 313 KYLWGFILFGWGLPAVFVAVVTVRATLANTECWDLSSGNKKWIIQVPIILAAIVNFIIF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTQRKQYRKLAKSTLVLVFVGVIYIVFVCLPHS 1244
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
Sbjct: 373 INIIRVLATKLRETNAGRCDFRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTW 446
+G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKGV A+R C+ NG+W+ + N+TW
Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVPCPDYIYDFNHHKGRAYRRCDNSGSEWELVPCNNRTW 161

Query: 447 ANYSDCLRFL 476
ANYS+C++FL
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677
++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
Match with FIG. 3 C

FIG. 3B

MATCH WITH FIG. 3B

Sbjct: 177 EREVFDRLGMIYTVGYSSISLGLTVAVLILGYFRRLLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740

KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNFNSFQGFVSIYCYCNGEVQAEVKKMWSRWNLSDWKRTPPCGS 1424

+G+ W+++MH E+ FNSFQGFV+IYC+CNGEVQAE+KK WSRW L++D+KR GS

Sbjct: 427 SGILWQVMHYEMLFNSFQGFVAIYCFNCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C